



SEQUENCE LISTING

<110> Sampath, Kuber T.
Cohen, Charles M.

<120> Methods For Tissue Morphogenesis and Methods for
Evaluating Morphogenic Activity

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<210> 1

<211> 1822

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (49)..(1341)

<223> "Morphogenic Protein OP-1"

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Met His Val
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cgc tca ctg cga gct gcg gcg ccg cac agc ttc gtg gcg ctc tgg gca 105
Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala
5 10 15

ccc ctg ttc ctg ctg cgc tcc gcc ctg gcc gac ttc agc ctg gac aac 153
Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn
20 25 30 35

gag gtg cac tcg agc ttc atc cac cgg cgc ctc cgc agc cag gag cgg 201
Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg
40 45 50

cgg gag atg cag cgc gag atc ctc tcc att ttg ggc ttg ccc cac cgc 249
Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg
55 60 65

ccg cgc ccg cac ctc cag ggc aag cac aac tcg gca ccc atg ttc atg 297
Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met
70 75 80

ctg gac ctg tac aac gcc atg gcg gtg gag gag ggc ggc ggg ccc ggc 345
Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly Gly Pro Gly
85 90 95

ggc cag ggc ttc tcc tac ccc tac aag gcc gtc ttc agt acc cag ggc 393

Gly	Gln	Gly	Phe	Ser	Tyr	Pro	Tyr	Lys	Ala	Val	Phe	Ser	Thr	Gln	Gly	
100					105					110					115	
ccc	cct	ctg	gcc	agc	ctg	caa	gat	agc	cat	ttc	ctc	acc	gac	gcc	gac	441
Pro	Pro	Leu	Ala	Ser	Leu	Gln	Asp	Ser	His	Phe	Leu	Thr	Asp	Ala	Asp	
				120					125					130		
atg	gtc	atg	agc	ttc	gtc	aac	ctc	gtg	gaa	cat	gac	aag	gaa	ttc	ttc	489
Met	Val	Met	Ser	Phe	Val	Asn	Leu	Val	Glu	His	Asp	Lys	Glu	Phe	Phe	
			135					140					145			
cac	cca	cgc	tac	cac	cat	cga	gag	ttc	cgg	ttt	gat	ctt	tcc	aag	atc	537
His	Pro	Arg	Tyr	His	His	Arg	Glu	Phe	Arg	Phe	Asp	Leu	Ser	Lys	Ile	
		150					155					160				
cca	gaa	ggg	gaa	gct	gtc	acg	gca	gcc	gaa	ttc	cgg	atc	tac	aag	gac	585
Pro	Glu	Gly	Glu	Ala	Val	Thr	Ala	Ala	Glu	Phe	Arg	Ile	Tyr	Lys	Asp	
	165					170				175						
tac	atc	cgg	gaa	cgc	ttc	gac	aat	gag	acg	ttc	cgg	atc	agc	gtt	tat	633
Tyr	Ile	Arg	Glu	Arg	Phe	Asp	Asn	Glu	Thr	Phe	Arg	Ile	Ser	Val	Tyr	
180					185					190					195	
cag	gtg	ctc	cag	gag	cac	ttg	ggc	agg	gaa	tcg	gat	ctc	ttc	ctg	ctc	681
Gln	Val	Leu	Gln	Glu	His	Leu	Gly	Arg	Glu	Ser	Asp	Leu	Phe	Leu	Leu	
			200						205					210		
gac	agc	cgt	acc	ctc	tgg	gcc	tcg	gag	gag	ggc	tgg	ctg	gtg	ttt	gac	729
Asp	Ser	Arg	Thr	Leu	Trp	Ala	Ser	Glu	Glu	Gly	Trp	Leu	Val	Phe	Asp	
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atc	aca	gcc	acc	agc	aac	cac	tgg	gtg	gtc	aat	ccg	cgg	cac	aac	ctg	777
Ile	Thr	Ala	Thr	Ser	Asn	His	Trp	Val	Val	Asn	Pro	Arg	His	Asn	Leu	
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ggc	ctg	cag	ctc	tcg	gtg	gag	acg	ctg	gat	ggg	cag	agc	atc	aac	ccc	825
Gly	Leu	Gln	Leu	Ser	Val	Glu	Thr	Leu	Asp	Gly	Gln	Ser	Ile	Asn	Pro	
	245					250					255					
aag	ttg	gcg	ggc	ctg	att	ggg	cgg	cac	ggg	ccc	cag	aac	aag	cag	ccc	873
Lys	Leu	Ala	Gly	Leu	Ile	Gly	Arg	His	Gly	Pro	Gln	Asn	Lys	Gln	Pro	
260					265					270					275	
ttc	atg	gtg	gct	ttc	ttc	aag	gcc	acg	gag	gtc	cac	ttc	cgc	agc	atc	921
Phe	Met	Val	Ala	Phe	Phe	Lys	Ala	Thr	Glu	Val	His	Phe	Arg	Ser	Ile	
				280					285					290		
cgg	tcc	acg	ggg	agc	aaa	cag	cgc	agc	cag	aac	cgc	tcc	aag	acg	ccc	969
Arg	Ser	Thr	Gly	Ser	Lys	Gln	Arg	Ser	Gln	Asn	Arg	Ser	Lys	Thr	Pro	
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aag	aac	cag	gaa	gcc	ctg	cgg	atg	gcc	aac	gtg	gca	gag	aac	agc	agc	1017
Lys	Asn	Gln	Glu	Ala	Leu	Arg	Met	Ala	Asn	Val	Ala	Glu	Asn	Ser	Ser	
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Ser	Asp	Gln	Arg	Gln	Ala	Cys	Lys	Lys	His	Glu	Leu	Tyr	Val	Ser	Phe	

325	330	335	
cga gac ctg ggc tgg cag gac tgg atc atc gcg cct gaa ggc tac gcc			1113
Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala			
340	345	350	355
gcc tac tac tgt gag ggg gag tgt gcc ttc cct ctg aac tcc tac atg			1161
Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met			
	360	365	370
aac gcc acc aac cac gcc atc gtg cag acg ctg gtc cac ttc atc aac			1209
Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn			
	375	380	385
ccg gaa acg gtg ccc aag ccc tgc tgt gcg ccc acg cag ctc aat gcc			1257
Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala			
	390	395	400
atc tcc gtc ctc tac ttc gat gac agc tcc aac gtc atc ctg aag aaa			1305
Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys			
405	410	415	
tac aga aac atg gtg gtc cgg gcc tgt ggc tgc cac tagctcctcc			1351
Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His			
420	425	430	
gagaattcag accctttggg gccaaagtttt tctggatcct ccattgctcg ccttggccag			1411
gaaccagcag accaactgcc ttttgtgaga ccttcccctc cctatcccca actttaagg			1471
tgtgagagta ttaggaaaca tgagcagcat atggcttttg atcagttttt cagtggcagc			1531
atccaatgaa caagatccta caagctgtgc aggcaaaacc tagcaggaaa aaaaaacaac			1591
gcataaagaa aaatggccgg gccaggtcat tggctgggaa gtctcagcca tgcacggact			1651
cgtttcaga ggtaattatg agcgcctacc agccaggcca cccagccgtg ggaggaagg			1711
ggcgtggcaa ggggtgggca cattggtgtc tgtgcgaaag gaaaattgac ccggaagttc			1771
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<211> 431			
<212> PRT			
<213> Homo sapiens			
<400> 2			
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Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser			
	20	25	30
Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser			
35	40	45	

Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu
 50 55 60
 Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro
 65 70 75 80
 Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly
 85 90 95
 Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser
 100 105 110
 Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr
 115 120 125
 Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys
 130 135 140
 Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu
 145 150 155 160
 Ser Lys Ile Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile
 165 170 175
 Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile
 180 185 190
 Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu
 195 200 205
 Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu
 210 215 220
 Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg
 225 230 235 240
 His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser
 245 250 255
 Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn
 260 265 270
 Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe
 275 280 285
 Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser
 290 295 300
 Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu
 305 310 315 320
 Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr
 325 330 335
 Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu
 340 345 350

Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn
 355 360 365

Ser Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His
 370 375 380

Phe Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln
 385 390 395 400

Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile
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Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
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<210> 3

<211> 102

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: OPX

<220>

<221> VARIANT

<222> (1)..(102)

<223> wherein each Xaa is independently selected from a
 group of one or more specified amino acids as
 defined in the specification

<400> 3

Cys Xaa Xaa His Glu Leu Tyr Val Ser Phe Xaa Asp Leu Gly Trp Xaa
 1 5 10 15

Asp Trp Xaa Ile Ala Pro Xaa Gly Tyr Xaa Ala Tyr Tyr Cys Glu Gly
 20 25 30

Glu Cys Xaa Phe Pro Leu Xaa Ser Xaa Met Asn Ala Thr Asn His Ala
 35 40 45

Ile Xaa Gln Xaa Leu Val His Xaa Xaa Xaa Pro Xaa Xaa Val Pro Lys
 50 55 60

Xaa Cys Cys Ala Pro Thr Xaa Leu Xaa Ala Xaa Ser Val Leu Tyr Xaa
 65 70 75 80

Asp Xaa Ser Xaa Asn Val Ile Leu Xaa Lys Xaa Arg Asn Met Val Val
 85 90 95

Xaa Ala Cys Gly Cys His
 100

<210> 4

<211> 97

<212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Generic
 Sequence 7

 <220>
 <221> VARIANT
 <222> (1)..(97)
 <223> wherein each Xaa is independently selected from a
 group of one or more specified amino acids defined
 in the specification

 <400> 4
 Leu Xaa Xaa Xaa Phe Xaa Xaa Xaa Gly Trp Xaa Xaa Trp Xaa Xaa Xaa
 1 5 10 15
 Pro Xaa Xaa Xaa Xaa Ala Xaa Tyr Cys Xaa Gly Xaa Cys Xaa Xaa Pro
 20 25 30
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn His Ala Xaa Xaa Xaa Xaa Xaa
 35 40 45
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Cys Xaa Pro
 50 55 60
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 65 70 75 80
 Val Xaa Leu Xaa Xaa Xaa Xaa Xaa Met Xaa Val Xaa Xaa Cys Xaa Cys
 85 90 95

 Xaa

<210> 5
 <211> 102
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Generic
 Sequence 8

<220>
 <221> VARIANT
 <222> ()..
 <223> wherein each Xaa is independently selected from a
 group of one or more specified amino acids defined
 in the specification

<400> 5
 Cys Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Phe Xaa Xaa Xaa Gly Trp Xaa
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa Ala Xaa Tyr Cys Xaa Gly
 20 25 30
 Xaa Cys Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn His Ala
 35 40 45
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 50 55 60
 Xaa Cys Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa
 65 70 75 80
 Xaa Xaa Xaa Xaa Xaa Val Xaa Leu Xaa Xaa Xaa Xaa Xaa Met Xaa Val
 85 90 95
 Xaa Xaa Cys Xaa Cys Xaa
 100

<210> 6
 <211> 97
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Generic
 Sequence 9

<220>
 <221> VARIANT
 <222> ()..
 <223> wherein each Xaa is independently selected from a
 group of one or more specified amino acids as
 defined in the specification

<400> 6
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10 15
 Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Gly Xaa Cys Xaa Xaa Xaa
 20 25 30
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 35 40 45
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Pro
 50 55 60
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa
 65 70 75 80
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Cys
 85 90 95
 Xaa

<210> 7
 <211> 102
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Generic
 Sequence 10

<220>
 <221> VARIANT
 <222> ()..)
 <223> wherein each Xaa is independently selected from a
 group of one or more specified amino acids as
 defined in the specification

<400> 7
 Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10 15
 Xaa Xaa Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Gly
 20 25 30
 Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 35 40 45
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 50 55 60
 Xaa Xaa Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa
 65 70 75 80
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 85 90 95
 Xaa Xaa Cys Xaa Cys Xaa
 100

<210> 8
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Peptide

<220>
 <221> VARIANT
 <222> (1)..(5)
 <223> wherein each Xaa is independently selected from a
 group of one or more specified amino acids as
 defined in the specification

<400> 8
 Cys Xaa Xaa Xaa Xaa

1

5

<210> 9

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peptide

<220>

<221> VARIANT

<222> (1)..(5)

<223> wherein each Xaa is independently selected from a
group of one or more specified amino acids as
defined in the specification

<400> 9

Cys Xaa Xaa Xaa Xaa

1

5